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November 6, 2004, 19:35:16; Search time 17.0625 Seconds (without alignments) 39.474 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                             283416 seqs, 96216763 residues
                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                          US-10-618-644-2
42
                                                                                                                                                                                                                                   1 PNNKPFQ 7
                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

SUMMARIES

glycinin G3 - soyb glycinin G3 precur glycinin chain A2B glycinin G2 precur glycinin G1 precur proportion Chain A1a glycinin G1 precur hemagglutinin precur hemagglutinin - in Description \$04605 \$11003 \$11002 \$11002 \$11002 \$11002 \$11002 \$10023 \$10033 \$1033 Query Match Length DB Score Result

hemagglutinin - in				hemagglutinin prec					hemagglutinin prec						
S52176	538637	HMIV15	HMIV33	HMIV77	HMIV86	HMIV89	HMIVS2	HMIV21	HMIV80	HMIV98	HMIVS3	JQ1154	301153	JQ1155	JQ1156
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347	362	550	550	550	550	550	550	550	550	550	550	550	550	550	250
88.1	88.1	88.1	88.1	88.1	88.1	88.1	88.1	88.1	88.1	88.1	88.1	88.1	88.1	88.1	88.1
_	_	_		37 88.1						37 88.1	37 88.1	37 88.1	37 88.1	37 88.1	37 88.1

ALIGNMENTS

RESULT 1

	giyeinin es - Boybean
	Cispecies: Glycine max (soybean)
	C;Date: 28-Feb-1990 #sequence_revision z8-Feb-1990 #text_cmange os-our-zoos
	C; Accession: S04605
_	
	Nucleic Acids Res. 17, 4388, 1989
	A; Title: The glycinin Gy(3) gene from soybean.
	A; Reference number: S04605; MUID: 89296500; PMID: 2740231
	A:Accession: S04605
	A:Molecule type: DNA
	*O+
	A. Cross_references iNIDROT: P11828; EMBL:X15123; NID:q18638; PIDN:CAA33217.1; PID:g1863
	Applemental source: variety our
	Aldene: Gy3
	A; Introne; 95/1; 1/1/5; 352/3
	Cjanberramiry: Grychiin
	100.0%;
	Best Local Similarity 100.0%; Fred. No. 1.3; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	Oy 1 PNNKPFQ 7
	Db 57 PNNKPPQ 63
	RESULT 2
	S11003
_	glycinin G3 precursor - soybean
	C. Aprenie G. Vicine max (Sovbean)
	C. Dare: 21-Nov-1993 #sequence revision 19-Jan-1996 #text change 03-May-1996
_	R; Nielsen, N.C.; Dickinson, C.D.; Cho, T.J.; Thanh, V.H.; Scallon, B.J.; Fischer, R.L
	Plant Cell 1, 313-328, 1989
	A, Title: Characterization of the glycinin gene family in soybean.
	A; Reference number: S10851; MUID:92393391; PMID:2485233
	A,Accession: S11003
	A; Molecule type: DNA
	A; Residues: 1-484 <nie></nie>
	A;Experimental source: variety Dare
	C;Genetics:
	A;Gene: Gy3
	C; Superfamily: glycinin
	C; Keywords: storage protein
	F:1-19/Domain: signal sequence #status predicted <sig></sig>
	F:20-484/Product: alveinin G3 #status predicted <mat></mat>
_	

100.0%; Score 42; DB 2; Length 484; 100.0%; Pred. No. 1.3;

Query Match Best Local Similarity

nemagglutinin

us-10-618-644-2.rpr

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Gaps

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C;Commant: Residues 297-300 and 481-485 are removed from the precursor during processing C;Commant: Residues 297-300 and 481-485 are removed from the precursor during processing C;Conetics:
A;Introns: 356/3
C;Superfamily: glycinin
C;Keywords: seed; storage protein
C;Keywords: seed; storage protein
C;Keywords: seed; storage protein
F;1-18/Domain: signal sequence #status predicted <SIG>F;1-18/Domain: signal sequence #status experimental <GLA>F;19-296/Product: glycinin chain Bla #status experimental <GLB>F;104-307/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glychin G2 precursor - soybean
N.Alternate names: glychin A2Bla
N.Alternate names: glychin A2Bla
N.Alternate names: glychin A2Bla
C.Becies: Glychne max (soybean)
A.Title: Characterization of the glychnin gene family in soybean.
A.Reference number: Sl0851; MUID:92393391; PMID:2485233
                                                                                                    A; Experimental source: seed C; Comment: Both acidic (A2) and basic (Bla) components of this glycinin subunit (A2Bla) disulfide bond.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding a glycinin A2Bla subunit pre
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A; Residues: 1-485 < THA>
A; Residues: 1-485 < THA>
A; Residues: 1-485 < THA>
A; Cross-references: EMBL:X15122; NID:g18636; PIDN:CAA33216.1; PID:g18637
A; Experimental source: variety Dare
B; Fukazawa, C.; Momma, T.; Higuchi, W.; Udaka, K.
Nucleic Acids Res. 15, 8117, 1987
A; Title: Complete nucleotide sequence of the gene encoding a glycinin A2E
A; Reference number: A26990; MUID:88040439; PMID:3671077
A; Accession: A26990
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A;Residues: 1-485 <NIE>
A;Residues: 1-485 <NIE>
A;Croses: Universes: Universes
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C;Superfamily: glycinin
C;Keywords: storage protein
E;1-18/Domain: signal sequence #status predicted <SIG>F;1-18/Product: glycinin G2 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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A,Residues: 1-485 <FUK>
A,Crose-references: GB:X02806
                         type: protein
118-132;205-215
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                           Alternate names: 11S globulin
N.Alternate names: 11S globulin
N.Alternate names: 11S globulin
N.Alternate names: 11S globulin
N.Alternate names: 11S globulin
C.Species: 31-War-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C.Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C.Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
R.Momma, T.; Negoro, T.; Udaka, K.; Fukazawa, C.
FEBS Lett. 188, 117-122, 1985
A.Title: A complete cDNA coding for the sequence of glycinin A2Bla subunit precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-485 A; Residues: 1-485 A; Ross-references: UNIPROT:P04405
A; Cross-references: UNIPROT:P04405
A; Experimental source: strain Bonmimori
A; Note: the source of this mRNA was cotyledon tissue taken from seeds at the middle stag
R; Marco, Y.A.; Thanh, V.H.; Tumer, N.E.; Scallon, B.J.; Nielsen, N.C.
A; Biol. Chem. 259, 113436-13441, 1984
A; Title: Cloning and structural analysis of DNA encoding an AzBla subunit of glycinin.
A; Reference number: A92454; MUID:85030472; PMID:6092376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. Mesidues: 19-38, '0', 40-60, 'S', 62-116, 'C', 118-192, 'E', 194-296;301-342, 'S', 344-463, 'I', 4 A. Residues: 19-38, 'D', 40-60, 'S', 62-116, 'C', 118-192, 'E', 194-296;301-342, 'S', 344-463, 'I', 4 A. Experimental source: strain CX635-1-1.

A. Note: residues 94-61y, 103-Asp, 195-61u, 318-Thr, 331-Val, 400-Asp and 400-Arg, 409-Va polypeptides differing slightly in their primary sequences

B. Staswick, P.E., Hermodson, M.A.; Nielsen, N.C.
J. Biol. Chem. 259, 13431-13435, 1984
A. Title: Identification of the cystines which link the acidic and basic components of the A. Title: Identification of the cystines which link the acidic and basic components of the A. Title: Identification of the Cystines which link the acidic and basic components of the A. Rikitamura, Y.; Arahira, M.; Itch, Y.; Fukazawa, C.

B. Kikitamura, Y.; Arahira, M.; Itch, Y.; Fukazawa, C.
A. Title: The complete nucleotide sequence of soybean glycinin A2Bla gene spanning to and A. Reference number: $10502; MUID:90332420; PMID:3377465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X53404; NID:g18522; PIDN:CAA37480.1; PID:g18524
R;Shutov, A.D.; Kakhovskaya, I.A.; Bastrygina, A.S.; Bulmaga, V.P.; Horstmann, C.; Muent
Br. J. Biochem. 241, 221-228, 1996
A;Title: Limited proteolysis of beta-conglycinin and glycinin, the 7S and 11S storage gl
A;Reference number: S74123; MUID:97054613; PMID:8898910
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               Gaps
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A;Residues: 318-485 < KM2>
A;Experimental source: strain CX635-1-1-1
R;Utsumi, S.; Kim, C.S.; Kohno, M.; Kito, M.
R;Utsumi, S. O.; Kohno, M.; Kito, M.
A;Atitle: Polymorphism and expression of cDNAs encoding glycinin subunits.
A;Reference number: A99024
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Y.Staswick, P.E.; Hermodson, M.A.; Nielsen, N.C.
I. Biol. (Chem. 259, 13424-13430, 1984
Y.Title: The amino acid sequence of the A2Bla subunit of glycinin.
          Indels
     ;
     Mismatches
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Residues: 1-38,'D',40-485 <UTS>
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A;Molecule type: DNA
A;Residues: 1-36 <KIT>
     Conservative
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PNNKPFQ 63
                                                                                               PNNKPFQ 7
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7;
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     Matches
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Gaps

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hemagglutinin - influenza A virus (strain SN1389 and IN0190)
C;Species: influenza A virus
C;Species: influenza A virus
C;Species: influenza A virus
C;Accession: J02275; J02376
R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J Gen. Virol. 74, 2513-2518, 1993
A;Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained A;Reference number: J02369; MUID: 94065682; PMID: 8245870
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C;Superfamily: influenza virus hemagglutinin; homotrimer; lipoprotein; thiolester bond
E;1-16/Domain: signal sequence #status predicted <816>
F;1-16/Domain: asgalutinin HA1 #status predicted <HA1>
F;345-556/Product: hemagglutinin HA2 #status predicted <HA2>
F;355-551/Domain: transmembrane #status predicted <TM1>
F;35-551/Domain: transmembrane #status predicted <TM1>
F;39-481,67-292,79-91,154-488,296-320/Disulfide bonds # #status predicted
F;357,53,78,180,300,498/Bainding site: carbohydrate (Asm) (covalent) #status predicted
F;554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hemagglutinin precursor - influenza A virus (strain A/equine/Uruguay/1/63[H3N8])
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
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C,Accession: A34064
R,Kawaoka, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
Virtle: Evolution of the hemagglutinin of equine H3 influenza viruses.
A,Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A,Reference number: A34064; WUID:89204899; PMID:2705299
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C;Superfamily: glydinin
C;Keywords: storage protein
F;1-19/Domain: signal sequence #status predicted <SIG>
P;20-495/Product: glycinin Gl #status predicted <WATI-
F;20-310/Product: glycinin Ala chain #status predicted <WATZ>
F;311-495/Product: glycinin Bx chain #status predicted <WATZ>
J. Agric. Food Chem. 35, 210-214, 1987
A;Title: An alternate cDNA encoding glycinin Ala Bx subunit.
A;Reference number: JS0015
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                                                                                                                           A,Accession: JS0015
A;Molecule type: mRNA
A;Regidues: 1-495 <UTS>
A;Experimental source: var. Shirotsurunoko
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100..
Lagarative
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Best Local Similarity 100.
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A;Molecule type: genomic RNA
A;Residues: 1-565 <KAW>
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PNNKPFQ 63
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A; Residues: 1-495 <NEGS-
A; Cross-references: UNIPROT: P04776; GB:X02985; NID:g18614; PIDN:CAA26723.1; PID:g18615
A; Cross-references: cv. Bonminori
A; Note: because of current nomenclature ambiguities, the authors choose to designate the
A; Note: because of current nomenclature ambiguities, the authors choose to designate the
R; Kitamura, Y; Arahira, M: Itoh, Y; Fukazawa, C.
Nucleic Acids Res. 18, 4245, 1990
A; Title: The complete nucleotide sequence of soybean glycinin A2B1a gene spanning to and
A; Reference number: $10502; MUID:90332420; PMID:2377465
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NyContains: glycinin chain AlaBx
NyContains: glycinin chain AlaBx
NyContains: glycinin chain AlaBy
NyContains: glycinin chain AlaBy
NyContains: glycinin chain AlaBy
Cispecies: Glycine max (soybean)
Cispecies: Glycinin gene family in soybean.
Arritle: Characterization of the glycinin gene family in soybean.
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A;Mactus: preliminary; translation not shown
A;Malecule type: DNA
A;Molecule type: DNA
CCOMMENT: The SULTE
C;Comment: The SOURCE of this protein was cotyledon tissue taken 38 days after flowering
C;Comment: By homology with the A2Bla component, residues 307-310, and 491-495 are remov
C;Superfamily: glycinin
C;Keywords: seed; storage protein
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                                                                                                                       glycinin chain AlaBx precursor - soybean
N.Alternate names: 11S globulin; glycinin AlaBlb
C;Species: Glycine max (soybean)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A23497; S10502
R;Negoro, T.; Momma, T.; Fukazawa, C.
Nucleic Acids Res. 13, 6719-6731, 1985
A;Title: A cDNA clone encoding a glycinin A-la subunit precursor of soybean.
A;Reference number: A23497; MUID:86041867; PMID:2997720
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A; Cross-references: UNIPROT: P04776
A; Cross-references: UNIPROT: P04776
A; Experimental source: variety Dare
B; Simm, T. L.; Goldberg, R.B.
Nucleic Acids Res: 17, 4386, 1989
A; Title: The glychin Gy(1) gene from soybean.
A; Reference number: S04603; MUID: 89296498; PMID: 2740229
A; Accession: S04603.
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A; Residues: 1-495 <SIM>
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us-10-618-644-2.rpr

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hemagglutinin - influenza A virus (isolate A/England/68/94) (fragment)
(Species influenza A virus
A;variety: isolate A/England/68/94
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
R;Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula A;Accession: S52173
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A;Residues: 1.347 <ELL.
A;Residues: 1.347 <ELL.
A;Cross-references: UNIPROT:082785; EMBL:Z46404; NID:g609045; PIDN:CAA86539.1; PID:g6090
A;Experimental source: 1solate A/England/68/94
C;Superfamily: influenza virus hemagglutinin
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C;Species: influenza A virus
C;Species: influenza A virus
A;Variety: isolate A/England/1/93
C;Bate: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S52175
R;Elis, J.S.
submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula A;Peference number: S52173
A;Molecule type: mRNA
A;Residues: 1-347 < ELLb.
A;Residues: 1-347 < ELLb.
A;Residues: 1-347 < ELLb.
A;Crosss-references: UNIPROT: Q82775; EMBL: Z46393; NID: g609024; PIDN: CAA86528.1; PID: g9405
C;Superfamily: influenza virus hemagglutinin
R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
J. Gen. Virol. 74, 2513-2518, 1993
J. Gen. Virol. 74, 2513-2518, 1993
A;Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained A;Reference number: JQ2377
A;Reference number: JQ2377
A;Molecule type: mRNA
A;Residues: 1-331 cROC>
A;Residues: 1-331 cROC>
A;Residues: 1-331 cROC>
A;Cross-references: UNIPROT:Q7LZX8; GB:L20105
A;Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
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                                                                                                                                                                                                                                                                                                        Length 331;
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Pred. No. 9.2;
1; Mismatches
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1es 6; Conservative
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291 PNDKPFQ 297
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289 PNDKPFQ 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                   C. Species: influenza A virus (strain SN1289)
C. Species: influenza A virus
C. Species: influenza A (HINI and H3N2) haemagglutinin sequences obtained
A. Title: Comparation of 10 influenza A (HINI and H3N2) haemagglutinin sequences obtained
A. Title: Comparation of 10 influenza A (HINI and H3N2) haemagglutinin sequences obtained
A. Recession: JQ2374
A. Residues: 1-330 «ROC»
A. Residues: 1-330 «ROC»
A. Coss-references: UNIRROT: O7LZYO; GB: L20115
A. Experimental source: subtype H3N2
C. Superfamily: influenza virus hemagglutinin
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C;Species: influenza A virus
C;Species: influenza A virus
C;Species: influenza A virus
C;Accession: J02378
B;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A;Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained A;Reference number: J02369; MUID:94065682; PMID:8245870
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C;Species: influenza A virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: JQ2377
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                                                                                                                                                         Length 330;
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85.7%; Pred. No. 8.7;
iive 1; Mismatches (
                                                                                                                                                 Query Match

88.1%; Score 37; DB 2

Best Local Similarity 85.7%; Pred. No. 8.7;

Matches 6; Conservative 1; Mismatches
             A,Residues: 1-330 <ROC>
A;Cross-references: UNIPROT:Q7LZX9; GB:L20119
A;Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
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A;Residues: 1-331 <ROC>
A;Cross-references: UNPROT:Q7LZX7; GB:L20102
A;Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
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Best Local Similarity 85.7
Matches 6; Conservative
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290 PNDKPFQ 296
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290 PNDKPFQ 296
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291 PNDKPFQ 297
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hemagglutinin - influenza A virus (isolate A/England/7/94) (fragment)
C;Species: influenza A virus
C;Species: influenza A virus
A;Variety: isolate A/England/7/94
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: 552187
R;Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula
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A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula
A;Description: Antigenic and genetic variation in the haemagglutinin
A;Cross-references: UNIPROT:Q82786; EMBL:Z46405; NID:g609047; PIDN:CAA86540.1; PID:g6090
A;Experimental source: isolate A/England/7/94
C;Superfamily: influenza virus hemagglutinin
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A,Residues: 1-347 <ELLD.
A,Cross-treferences: UNIPROT:Q82782; EMBL:Z46401; NID:g609039; PIDN:CAA86536.1; PID:g6090
A;Experimental source: isolate A/England/347/93
C;Superfamily: influenza virus hemagglutinin
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tive 1; Mismatches 0; Indels
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